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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/352,570A

DATE: 10/10/2002
 TIME: 10:08:28

Input Set : A:\00398.506001.SEQLIST.TXT
 Output Set: N:\CRF4\10102002\I352570A.raw

4 <110> APPLICANT: Michael E. Mendelsohn
 7 <120> TITLE OF INVENTION: METHOD FOR ASSAYING COMPOUNDS AFFECTING
 8 CELL DIVISION
 10 <130> FILE REFERENCE: 00398/506001
 12 <140> CURRENT APPLICATION NUMBER: 09/352,570A
 13 <141> CURRENT FILING DATE: 1999-07-13
 15 <160> NUMBER OF SEQ ID NOS: 7
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 618
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)...(618)
 28 <400> SEQUENCE: 1
 29 atg gcg ctg cag ctc tcc cgg gag cag gga atc acc ctc cgc ggg agc 48
 30 Met Ala Leu Gln Leu Ser Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser
 31 1 5 10 15
 33 gcc gaa atc gtg gcc gag ttc ttc tca ttc ggc atc aac agc att tta 96
 34 Ala Glu Ile Val Ala Glu Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu
 35 20 25 30
 37 tat cag cgt ggc ata tat cca tct gaa acc ttt act cga gtg cag aaa 144
 38 Tyr Gln Arg Gly Ile Tyr Pro Ser Glu Thr Phe Thr Arg Val Gln Lys
 39 35 40 45
 41 tac gga ctc acc ttg ctt gta act act gat ctt gag ctc ata aaa tac 192
 42 Tyr Gly Leu Thr Leu Leu Val Thr Thr Asp Leu Glu Leu Ile Lys Tyr
 43 50 55 60
 45 cta aat aat gtg gtg gaa caa ctg aaa gat tgg tta tac aag tgt tca 240
 46 Leu Asn Asn Val Val Glu Gln Leu Lys Asp Trp Leu Tyr Lys Cys Ser
 47 65 70 75 80
 49 gtt cag aaa ctg gtt gta atc tca aat att gaa agt ggt gag gtc 288
 50 Val Gln Lys Leu Val Val Ile Ser Asn Ile Glu Ser Gly Glu Val
 51 85 90 95
 53 ctg gaa aga tgg cag ttt gat att gag tgt gac aag act gca aaa gat 336
 54 Leu Glu Arg Trp Gln Phe Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp
 55 100 105 110
 57 gac agt gca ccc aga gaa aag tct cag aaa gct atc cag gat gaa atc 384
 58 Asp Ser Ala Pro Arg Glu Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile
 59 115 120 125
 61 cgt tca gtg atc aga cag atc aca gct acg gtg aca ttt ctg cca ctg 432
 62 Arg Ser Val Ile Arg Gln Ile Thr Ala Thr Val Thr Phe Leu Pro Leu
 63 130 135 140

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65 ttg gaa gtt tct tgt tca ttt gat ctg ctg att tat aca gac aaa gat    480
66 Leu Glu Val Ser Cys Ser Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp
67 145          150          155          160
69 ttg gtt gta cct gaa aaa tgg gaa gag tcg gga cca cag ttt att acc    528
70 Leu Val Val Pro Glu Lys Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr
71          165          170          175
73 aat tct gag gaa gtg cgc ctt cgt tca ttt act act aca atc cac aaa    576
74 Asn Ser Glu Glu Val Arg Leu Arg Ser Phe Thr Thr Ile His Lys
75          180          185          190
77 gta aat agc atg gtg gcc tac aaa att cct gtc aat gac tga             618
78 Val Asn Ser Met Val Ala Tyr Lys Ile Pro Val Asn Asp   *
79          195          200          205
83 <210> SEQ ID NO: 2
84 <211> LENGTH: 199
85 <212> TYPE: PRT
86 <213> ORGANISM: Homo sapiens
88 <400> SEQUENCE: 2
89 Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu Ile Val Ala Glu
90 1          5          10          15
91 Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln Arg Gly Ile Tyr
92          20          25          30
93 Pro Ser Glu Thr Phe Thr Arg Val Gln Lys Tyr Gly Leu Thr Leu Leu
94          35          40          45
95 Val Thr Thr Asp Leu Glu Leu Ile Lys Tyr Leu Asn Asn Val Val Glu
96          50          55          60
97 Gln Leu Lys Asp Trp Leu Tyr Lys Cys Ser Val Gln Lys Leu Val Val
98 65          70          75          80
99 Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu Glu Arg Trp Gln Phe
100          85          90          95
101 Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser Ala Pro Arg Glu
102          100         105         110
103 Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser Val Ile Arg Gln
104          115         120         125
105 Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu Glu Val Ser Cys Ser
106          130         135         140
107 Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val Val Pro Glu Lys
108 145          150          155          160
109 Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser Glu Glu Val Arg
110          165          170          175
111 Leu Arg Ser Phe Thr Thr Ile His Lys Val Asn Ser Met Val Ala
112          180          185          190
113 Tyr Lys Ile Pro Val Asn Asp
114          195
117 <210> SEQ ID NO: 3
118 <211> LENGTH: 600
119 <212> TYPE: DNA
120 <213> ORGANISM: Ovis aries
122 <220> FEATURE:
123 <221> NAME/KEY: CDS

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124 <222> LOCATION: (1)...(600)
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128 Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu Ile Val Ala Glu
129 1 5 10 15
131 ttc ttc tca ttt ggt atc aac agt att tta tat cag cgt ggc ata tat 96
132 Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln Arg Gly Ile Tyr
133 20 25 30
135 cca tcg gaa acc ttt act cga gtg cag aaa tat gga ctc acc ttg ctt 144
136 Pro Ser Glu Thr Phe Thr Arg Val Gln Lys Tyr Gly Leu Thr Leu Leu
137 35 40 45
139 gta act act gat cct gag ctc ata aaa tac cta aat aat gtg gtg gat 192
140 Val Thr Thr Asp Pro Glu Leu Ile Lys Tyr Leu Asn Asn Val Val Asp
141 50 55 60
143 caa cta aaa gaa tgg tta tac aag tgt tca gtt cag aaa ctg gtg gta 240
144 Gln Leu Lys Glu Trp Leu Tyr Lys Cys Ser Val Gln Lys Leu Val Val
145 65 70 75 80
147 gtc atc tca aat att gaa agt gga gag gtc ctt gaa aga tgg cag ttt 288
148 Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu Glu Arg Trp Gln Phe
149 85 90 95
151 gat att gag tgt gac aag act gca aaa gat gac agt gca ccc aga gaa 336
152 Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser Ala Pro Arg Glu
153 100 105 110
155 aag tct cag aaa gct atc caa gat gaa atc cgt tca gtg atc aga cag 384
156 Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser Val Ile Arg Gln
157 115 120 125
159 atc aca gct aca gta aca ttt ctg cca ctg ttg gaa gtt tct tgt tca 432
160 Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu Glu Val Ser Cys Ser
161 130 135 140
163 ttt gat ctc ctc att tat aca gac aaa gat ctg gtt gta cct gag aaa 480
164 Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val Val Pro Glu Lys
165 145 150 155 160
167 tgg gaa gag tcc gga cca cag ttc att acc aat tct gaa gaa gtt cgt 528
168 Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser Glu Glu Val Arg
169 165 170 175
171 ctt cgt tca ttc act act aca att cac aaa gta aat agc atg gta gcc 576
172 Leu Arg Ser Phe Thr Thr Ile His Lys Val Asn Ser Met Val Ala
173 180 185 190
175 tac aaa att cct gtc cat gac tga 600
176 Tyr Lys Ile Pro Val His Asp *
177 195
180 <210> SEQ ID NO: 4
181 <211> LENGTH: 199
182 <212> TYPE: PRT
183 <213> ORGANISM: Ovis aries
185 <400> SEQUENCE: 4
186 Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu Ile Val Ala Glu
187 1 5 10 15
188 Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln Arg Gly Ile Tyr

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189          20          25          30
190 Pro Ser Glu Thr Phe Thr Arg Val Gln Lys Tyr Gly Leu Thr Leu Leu
191          35          40          45
192 Val Thr Thr Asp Pro Glu Leu Ile Lys Tyr Leu Asn Asn Val Val Asp
193          50          55          60
194 Gln Leu Lys Glu Trp Leu Tyr Lys Cys Ser Val Gln Lys Leu Val Val
195          65          70          75          80
196 Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu Glu Arg Trp Gln Phe
197          85          90          95
198 Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser Ala Pro Arg Glu
199          100         105         110
200 Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser Val Ile Arg Gln
201          115         120         125
202 Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu Glu Val Ser Cys Ser
203          130         135         140
204 Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val Val Pro Glu Lys
205          145         150         155         160
206 Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser Glu Glu Val Arg
207          165         170         175
208 Leu Arg Ser Phe Thr Thr Ile His Lys Val Asn Ser Met Val Ala
209          180         185         190
210 Tyr Lys Ile Pro Val His Asp
211          195
214 <210> SEQ ID NO: 5
215 <211> LENGTH: 1458
216 <212> TYPE: DNA
217 <213> ORGANISM: Mus musculus
219 <400> SEQUENCE: 5
220 atggcattct acagtccgtc ttttatgttac tacagtgttc ccagcagcac cggttaacctg 60
221 gaagggtggc ctgttgcaca gactgcaagc ccaaattgtgc tatggccaaac ttctggacac 120
222 ctctctccct tagccaccca ctgccaatca tcgtttctct atgcagaacc taaaagagt 180
223 ccttgggtgt aagcaagatc actagaaacac accttgcctg taaacagaga gaccctgaag 240
224 aggaagcttg gcgggagcgg ttgtgccagc cctgttacta gtccaaagcac caagagggat 300
225 gctcaattct gtgccgtctg cagtgttatttgcatctgggt atcattacgg tgctctggtcc 360
226 tgtgaaggat gtaaggcctt ttttaaaaga agcattcaag gacataatga ctatatctgt 420
227 ccagccacga atcagtgtac gatagacaag aaccggcgta aaaactgcca ggcctgccc 480
228 cttcgcaagt gttacgaagt aggaatggtc aagtgtggat ccaggagaga aaggtgtggg 540
229 taccgaatag tacgaagaca gagaagtgcc agcgagcagg tgcattgcct gaacaaagcc 600
230 aagagaacca gtgggcacac accccgggtt aaggagctac tgctgaactc tctgagtccc 660
231 gagcagctgg tgctcaccct gcttggaaatc gaggccatca atgtgttagt gagtcgtccc 720
232 agcatgcctt tcaccggaggc ctccatgtat atgtccctta cgaagctggc tgacaaggaa 780
233 ctgggtcaca tgattggctg ggccaaagaaa atccctggct ttgtggagct cagcctgttg 840
234 gaccaagtcc gccttggaa aagctgtgg atggaggtgc tgatgggtgg gctgatgtgg 900
235 cgctccatcg accaccccg caagctcatc tttgctccag acctcgatct ggacagggat 960
236 gaggggaagt gcgttggaaagg gattctggaa atcttgaca tgctccttgc gacgacggca 1020
237 cggttccgtg agttaaaact gcagcacaaa gaatatctgt gtgtgaaggc catgattctc 1080
238 ctcaactcca gtatgtacca cttggctacc gcaagccagg aagcagagag tagccggaaag 1140
239 ctgacacacc tattgaacgc agtgcacat gcccgttgc gggtgatttc gaagagtaga 1200
240 atctctcccc agcagcagtc agtccgtctg gccaacctcc tgatgtttct ttctcatgtc 1260

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241 aggacacatca gtaacaaggg catggaacat ctgctcagca tgaagtgc aaatgtggtc 1320
 242 cccgtgtacg acctgctgct ggagatgcg aatgctaca cgcttcgagg gtacaagtcc 1380
 243 tcaatctcg ggtctgggtg ctgctcgaca gaggacagta agagcaaaga gggctcccag 1440
 244 aacctccagt ctcagtga 1458
 246 <210> SEQ ID NO: 6
 247 <211> LENGTH: 485
 248 <212> TYPE: PRT
 249 <213> ORGANISM: Mus musculus
 251 <400> SEQUENCE: 6
 252 Met Ala Phe Tyr Ser Pro Ala Val Met Asn Tyr Ser Val Pro Ser Ser
 253 1 5 10 15
 254 Thr Gly Asn Leu Glu Gly Gly Pro Val Arg Gln Thr Ala Ser Pro Asn
 255 20 25 30
 256 Val Leu Trp Pro Thr Ser Gly His Leu Ser Pro Leu Ala Thr His Cys
 257 35 40 45
 258 Gln Ser Ser Leu Leu Tyr Ala Glu Pro Gln Lys Ser Pro Trp Cys Glu
 259 50 55 60
 260 Ala Arg Ser Leu Glu His Thr Leu Pro Val Asn Arg Glu Thr Leu Lys
 261 65 70 75 80
 262 Arg Lys Leu Gly Gly Ser Gly Cys Ala Ser Pro Val Thr Ser Pro Ser
 263 85 90 95
 264 Thr Lys Arg Asp Ala His Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser
 265 100 105 110
 266 Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe
 267 115 120 125
 268 Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Ile Cys Pro Ala Thr Asn
 269 130 135 140
 270 Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Asn Cys Gln Ala Cys Arg
 271 145 150 155 160
 272 Leu Arg Lys Cys Tyr Glu Val Gly Met Val Lys Cys Gly Ser Arg Arg
 273 165 170 175
 274 Glu Arg Cys Gly Tyr Arg Ile Val Arg Arg Gln Arg Ser Ala Ser Glu
 275 180 185 190
 276 Gln Val His Cys Leu Asn Lys Ala Lys Arg Thr Ser Gly His Thr Pro
 277 195 200 205
 278 Arg Val Lys Glu Leu Leu Leu Asn Ser Leu Ser Pro Glu Gln Leu Val
 279 210 215 220
 280 Leu Thr Leu Leu Glu Ala Glu Pro Pro Asn Val Leu Val Ser Arg Pro
 281 225 230 235 240
 282 Ser Met Pro Phe Thr Glu Ala Ser Met Met Met Ser Leu Thr Lys Leu
 283 245 250 255
 284 Ala Asp Lys Glu Leu Val His Met Ile Gly Trp Ala Lys Lys Ile Pro
 285 260 265 270
 286 Gly Phe Val Glu Leu Ser Leu Leu Asp Gln Val Arg Leu Leu Glu Ser
 287 275 280 285
 288 Cys Trp Met Glu Val Leu Met Val Gly Leu Met Trp Arg Ser Ile Asp
 289 290 295 300
 290 His Pro Gly Lys Leu Ile Phe Ala Pro Asp Leu Val Leu Asp Arg Asp
 291 305 310 315 320

VERIFICATION SUMMARY

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